Figure 1a / 3

SEQ ID NO:1

```
  1 MILSLLFSLG GPLGWGLLGA WAQASSTSLS DLQSSRTPGV WKAEAEDTGK DPVGRNWCPY
 61 PMSKLVTLLA LCKTEKFLIH SQQPCPQGAP DCQKVKVMYR MAHKPVYQVK QKVLTSLAWR
121 CCPGYTGPNC EHHDSMAIPE PADPGDSHQE PQDGPVSFKP GHLAAVINEV EVQQEQQEHL
181 LGDLQNDVHR VADSLPGLWK ALPGNLTAAS LSNDVKNVGR CCEAEAGAGA ASLNASLHGL
241 HNALFATQRS LEQHQRLFHS LFGNFQGLME ANVSLDLGKL QTMLSRKGKK QQKDLEAPRK
301 RDKKEAEPLV DIRVTGPVPG ALGAALWEAG SPVAFYASFS EGTAALQTVK FNTTYINIGS
361 SYFPEHGYFR APERGVYLFA VSVEFGPGPG TGQLVFGGHH RTPVCTTGQG SGSTATVFAM
421 AELQKGERVW FELTQGSITK RSLSGTAFGG FLMFKT
```

SEQ ID NO:2

```
  1 ASSTSLSDLQ SSRTPGVWKA EAEDTSKDPV GRNWCPYPMS KLVTLLALCK TEKFLIHSQQ
 61 PCPQGAPDCQ KVKVMYRMAH KPVYQVKQKV LTSLAWRCCP GYTGPNCEHH DSMAIPEPAD
121 PGDSHQEPQD GPVSFKPGHL AAVINEVEVQ QEQQEHLLGD LQNDVHRVAD SLPGLWKALP
181 GNLTAASLSN DVKNVGRCCE AEAGAGAASL NASLHGLHNA LFATQRSLEQ HQRLFHSLFG
241 NFQGLMEANV SLDLGKLQTM LSRKGKKQQK DLEAPRKRDK KEAEPLVDIR VTGPVPGALG
301 AALWEAGSPV AFYASFSEGT AALQTVKFNT TYINIGSSYF PEHGYFRAPE RGVYLFAVSV
361 EFGPGPGTGQ LVFGGHHRTP VCTTGQGSGS TATVFAMAEL QKGERVWFEL TQGSITKRSL
421 SGTAFGGFLM FKT
```

SEQ ID NO:3

```
  1 EAEPLVDIRV TGPVPGALGA ALWEAGSPVA FYASFSEGTA ALQTVKFNTT YINIGSSYFP
 61 EHGYFRAPER GVYLFAVSVE FGPGPGTGQL VFGGHHRTPV CTTGQGSGST ATVFAMAELQ
121 KGERVWFELT QGSITKRSLS GTAFGGFLMF KT
```

SEQ ID NO:4

```
TPVCTTGQGS GSTATVFAMA ELQK
```

SEQ ID NO:5

```
VWFELTQGSI TK
```

SEQ ID NO:6

```
SLSGTAFGGF LMFK
```

Figure 1b / 3

SEQ ID NO:7

```
   1 atgatcctgagcttgctgttcagccttgggggccccctgggctgggggctgctgggggca
  61 tgggcccaggcttccagtactagcctctctgatctgcagagctccaggacacctggggtc
 121 tggaaggcagaggctgaggacaccggcaaggaccccgtaggacgtaactggtgcccctac
181 ccaatgtccaagctggtcaccttactagctctttgcaaaacagagaaattcctcatccac
241 tcgcagcagccgtgtccgcagggagctccagactgccagaaagtcaaagtcatgtaccgc
301 atggcccacaagccagtgtaccaggtcaagcagaaggtgctgacctctttggcctggagg
361 tgctgccctggctacacgggccccaactgcgagcaccacgattccatggcaatccctgag
421 cctgcagatcctggtgacagccaccaggaacctcaggatggaccagtcagcttcaaacct
481 ggccaccttgctgcagtgatcaatgaggttgaggtgcaacaggaacagcaggaacatctg
541 ctgggagatctccagaatgatgtgcaccgggtggcagacagcctgccaggcctgtggaaa
601 gccctgcctggtaacctcacagctgcaagcctgagcaacgacgtcaagaatgtcgggcgg
661 tgctgcgaggccgaggccggggccggggccgcctccctcaacgcctcccttcacggcctc
721 cacaacgcactcttcgccactcagcgcagcttggagcagcaccagcggctcttccacagc
781 ctctttgggaacttccaagggctcatggaagccaacgtcagcctggacctggggaagctg
841 cagaccatgctgagcaggaaagggaagaagcagcagaaagacctggaagctccccggaag
901 agggacaagaaggaagcggagcctttggtggacatacgggtcacagggcctgtgccaggt
961 gccttgggcgcggcgctctgggaggcaggatcccctgtggccttctatgccagcttttca
1021 gaagggacggctgccctgcagacagtgaagttcaacaccacatacatcaacattggcagc
1081 agctacttccctgaacatggctacttccgagcccctgagcgtggtgtctacctgtttgca
1141 gtgagcgttgaatttggcccagggccaggcaccgggcagctggtgtttggaggtcaccat
1201 cggactccagtctgtaccactgggcaggggagtggaagcacagcaacggtctttgccatg
1261 gctgagctgcagaagggtgagcgagtatggtttgagttaacccagggatcaataacaaag
1321 agaagcctgtcgggcactgcatttgggggcttcctgatgtttaagacctga
```

Figure 2a / 3

```
          10         20         30         40         50         60
ATGATCCTGAGCTTGCTGTTCAGCCTTGGGGGCCCCCTGGGCTGGGGGCTGCTGGGGGCA
 M  I  L  S  L  L  F  S  L  G  G  P  L  G  W  G  L  L  G  A

          70         80         90         100        110        120
TGGGCCCAGGCTTCCAGTACTAGCCTCTCTGATCTGCAGAGCTCCAGGACACCTGGGGTC
 W  A  Q  A  S  S  T  S  L  S  D  L  Q  S  S  R  T  P  G  V

          130        140        150        160        170        180
TGGAAGGCAGAGGCTGAGGACACCGGCAAGGACCCCGTAGGACGTAACTGGTGCCCCTAC
 W  K  A  E  A  E  D  T  G  K  D  P  V  G  R  N  W  C  P  Y

          190        200        210        220        230        240
CCAATGTCCAAGCTGGTCACCTTACTAGCTCTTTGCAAAACAGAGAAATTCCTCATCCAC
 P  M  S  K  L  V  T  L  L  A  L  C  K  T  E  K  F  L  I  H

          250        260        270        280        290        300
TCGCAGCAGCCGTGTCCGCAGGGAGCTCCAGACTGCCAGAAAGTCAAAGTCATGTACCGC
 S  Q  Q  P  C  P  Q  G  A  P  D  C  Q  K  V  K  V  M  Y  R

          310        320        330        340        350        360
ATGGCCCACAAGCCAGTGTACCAGGTCAAGCAGAAGGTGCTGACCTCTTTGGCCTGGAGG
 M  A  H  K  P  V  Y  Q  V  K  Q  K  V  L  T  S  L  A  W  R

          370        380        390        400        410        420
TGCTGCCCTGGCTACACGGGCCCCAACTGCGAGCACCACGATTCCATGGCAATCCCTGAG
 C  C  P  G  Y  T  G  P  N  C  E  H  H  D  S  M  A  I  P  E

          430        440        450        460        470        480
CCTGCAGATCCTGGTGACAGCCACCAGGAACCTCAGGATGGACCAGTCAGCTTCAAACCT
 P  A  D  P  G  D  S  H  Q  E  P  Q  D  G  P  V  S  F  K  P

          490        500        510        520        530        540
GGCCACCTTGCTGCAGTGATCAATGAGGTTGAGGTGCAACAGGAACAGCAGGAACATCTG
 G  H  L  A  A  V  I  N  E  V  E  V  Q  Q  E  Q  Q  E  H  L

          550        560        570        580        590        600
CTGGGAGATCTCCAGAATGATGTGCACCGGGTGGCAGACAGCCTGCCAGGCCTGTGGAAA
 L  G  D  L  Q  N  D  V  H  R  V  A  D  S  L  P  G  L  W  K

          610        620        630        640        650        660
GCCCTGCCTGGTAACCTCACAGCTGCAAGCCTGAGCAACGACGTCAAGAATGTCGGGCGG
 A  L  P  G  N  L  T  A  A  S  L  S  N  D  V  K  N  V  G  R

          670        680        690        700        710        720
TGCTGCGAGGCCGAGGCCGGGGCCGGGGCCGCCTCCCTCAACGCCTCCCTTCACGGCCTC
 C  C  E  A  E  A  G  A  G  A  A  S  L  N  A  S  L  H  G  L

          730        740        750        760        770        780
CACAACGCACTCTTCGCCACTCAGCGCAGCTTGGAGCAGCACCAGCGGCTCTTCCACAGC
 H  N  A  L  F  A  T  Q  R  S  L  E  Q  H  Q  R  L  F  H  S

          790        800        810        820        830        840
CTCTTTGGGAACTTCCAAGGGCTCATGGAAGCCAACGTCAGCCTGGACCTGGGGAAGCTG
 L  F  G  N  F  Q  G  L  M  E  A  N  V  S  L  D  L  G  K  L

          850        860        870        880        890        900
CAGACCATGCTGAGCAGGAAAGGGAAGAAGCAGCAGAAAGACCTGGAAGCTCCCCGGAAG
 Q  T  M  L  S  R  K  G  K  K  Q  Q  K  D  L  E  A  P  R  K

          910        920        930        940        950        960
AGGGACAAGAAGGAAGCGGAGCCTTTGGTGGACATACGGGTCACAGGGCCTGTGCCAGGT
 R  D  K  K  E  A  E  P  L  V  D  I  R  V  T  G  P  V  P  G
```

Figure 2b / 3

```
         970        980        990        1000       1010       1020
GCCTTGGGCGCGGCGCTCTGGGAGGCAGGATCCCCTGTGGCCTTCTATGCCAGCTTTTCA
 A  L  G  A  A  L  W  E  A  G  S  P  V  A  F  Y  A  S  F  S

         1030       1040       1050       1060       1070       1080
GAAGGGACGGCTGCCCTGCAGACAGTGAAGTTCAACACCACATACATCAACATTGGCAGC
 E  G  T  A  A  L  Q  T  V  K  F  N  T  T  Y  I  N  I  G  S

         1090       1100       1110       1120       1130       1140
AGCTACTTCCCTGAACATGGCTACTTCCGAGCCCCTGAGCGTGGTGTCTACCTGTTTGCA
 S  Y  F  P  E  H  G  Y  F  R  A  P  E  R  G  V  Y  L  F  A

         1150       1160       1170       1180       1190       1200
GTGAGCGTTGAATTTGGCCCAGGGCCAGGCACCGGGCAGCTGGTGTTTGGAGGTCACCAT
 V  S  V  E  F  G  P  G  P  G  T  G  Q  L  V  F  G  G  H  H

         1210       1220       1230       1240       1250       1260
CGGACTCCAGTCTGTACCACTGGGCAGGGGAGTGGAAGCACAGCAACGGTCTTTGCCATG
 R  T  P  V  C  T  T  G  Q  G  S  G  S  T  A  T  V  F  A  M

         1270       1280       1290       1300       1310       1320
GCTGAGCTGCAGAAGGGTGAGCGAGTATGGTTTGAGTTAACCCAGGGATCAATAACAAAG
 A  E  L  Q  K  G  E  R  V  W  F  E  L  T  Q  G  S  I  T  K

         1330       1340       1350       1360       1370
AGAAGCCTGTCGGGCACTGCATTTGGGGGCTTCCTGATGTTTAAGACCTGA
 R  S  L  S  G  T  A  F  G  G  F  L  M  F  K  T  *
```

Figure 3 / 3

CLUSTAL W (1.81) multiple sequence alignment of SEQ ID NO:1 and Q8K1Z7 (murine homolog)

```
SEQ ID NO:1 MILSLLFSLGGPLGWGLLGAWAQASSTSLSDLQSSRTPGVWKAEAEDTGKDPVGRNWCPY
Q8K1Z7      MIPTLLLGFGVYLSWGLLGSWAQDPGTKFSHLNRPGMPEGWRLGAEDTSRDPIRRNWCPY
            ** :**:.:*  *.*****:*** ..*.:*.*: .  *  *:  ****.:**: ******

SEQ ID NO:1 PMSKLVTLLALCKTEKFLIHSQQPCPQGAPDCQKVKVMYRMAHKPVYQVKQKVLTSLAWR
Q8K1Z7      QKSRLVTFVAACKTEKFLVHSQQPCPQGAPDCQGVRVMYRVAQKPVYQVQQKVLISVDWR
            *:***::* *******:************** *:****:*:******:**** *: **

SEQ ID NO:1 CCPGYTGPNCEHHDSMAIPEPADPGDSHQEPQDGPVSFKPGHLAAVINEVEVQQEQQEHL
Q8K1Z7      CCPGFQGPDCQDHNPTANPEPTEPSGKLQETWDSMDGFELGHPVPEFNEIKVPQEQQE--
            ****: **:*:.*:. * ***::*... **. *.  .*: ** .. :**::* *****

SEQ ID NO:1 LGDLQNDVHRVADSLPGLWKALPGNLTAASLSNDVKNVGRCCEAEAGAGAASLNASLHGL
Q8K1Z7      ----------------------------IRRLSSDVKQIGQCCEASW---AASLNSSLEDL
                                         **.***::*:****.    *****:**..*

SEQ ID NO:1 HNALFATQRSLEQHQRLFHSLFGNFQGLMEANVSLDLGKLQTMLSRKGKKQQKDLEAPRK
Q8K1Z7      HSMLLDTQHGLRQHRQLFHNLFQNFQGLVASNISLDLGKLQAMLSKKDKKQPRGPGESRK
            *. *: **:.*.**::***.** *****: :*:********:***:*.*** :.   .**

SEQ ID NO:1 RDKKEAEPLVDIRVTGPVPGALGAALWEAGSPVAFYASFSEGTAALQTVKFNTTYYINIGS
Q8K1Z7      RDKKQVVMSTDAHAKG-------LELWETGSPVAFYAGSSEGATALQMVKFNTTSINVGS
            ****:.   .* :..*         ***:********. ***::*** ****** **:**

SEQ ID NO:1 SYFPEHGYFRAPERGVYLFAVSVEFGPGPGTGQLVFGGHHRTPVCTTGQGSGSTATVFAM
Q8K1Z7      SYFPEHGYFRAPKRGVYLFAVSITFGPGPGMGQLVFEGHHRVPVYSTEQRGGSTATTFAM
            ************:*********: ****** ***** ****.** :* * .*****.***

SEQ ID NO:1 AELQKGERVWFELTQGSITKRSLSGTAFGGFLMFKT
Q8K1Z7      VELQKGERAWFELIQGSATKGSQPGTAFGGFLMFKT
            .*******.**** *** ** * .************
```